



#14

SEQUENCE LISTING

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Wong, Geraldine S.
Rodriguez, Henry

<120> COMPOSITIONS AND METHODS FOR DETECTING STRESS-INDUCIBLE PROTEINS

<130> 12071-006001

<140> US 09/733,179

<141> 2000-12-07

<150> WO USOO/33341

<151> 2000-12-07

<150> US 60/169,535

<151> 1999-12-07

<160> 15

<170> FastSEQ for Windows Version 4.0

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<211> 21

<212> PRT

<213> Homo sapiens

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Ser Thr Gly Pro Ile
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Cys Gly Thr Gln Ala Arg Gln Gly Asp Pro Ser Thr Gly Pro Ile
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<213> Homo sapiens

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Cys Gly Thr Gln Ala Arg Gln Gly Asp Pro Ser Thr
1 5 10

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Arg Asp Lys Ile Pro Glu Glu Asp Arg Arg Lys Met Gln Asp Lys Cys
 1 5 10 15

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Arg Asp Lys Ile Pro Glu Glu Asp Arg Arg Lys Met Gln
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<213> Homo sapiens

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Ala His Val Phe His Val Lys Gly Ser Leu Gln Glu Glu Ser Leu Arg
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 Asp Lys Ile Pro Glu Glu Asp Arg Arg Lys Met Gln
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Ala His Val Phe His Val Lys Gly Ser Leu Gln Glu Glu Ser
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<210> 8

<211> 12

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Met Gln Ala Pro Arg Glu Leu Ala Val Gly Ile Asp
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<210> 9

<211> 13

<212> PRT

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Met Gln Ala Pro Arg Glu Leu Ala Val Gly Ile Asp Cys
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<213> Homo sapiens

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Gly	Ser	Leu	Gln	Glu	Glu	Ser	Leu	Arg	Asp	Lys	Ile	Pro	Glu	Glu
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Met	Gln	Ala	Pro	Arg	Glu	Leu	Ala	Val	Gly	Ile	Asp	Leu	Gly	Thr	Thr
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Tyr	Ser	Cys	Val	Gly	Val	Phe	Gln	Gln	Gly	Arg	Val	Glu	Ile	Leu	Ala
			20					25					30		
Asn	Asp	Gln	Gly	Asn	Arg	Thr	Thr	Pro	Ser	Tyr	Val	Ala	Phe	Thr	Asp
		35					40					45			
Thr	Glu	Arg	Leu	Val	Gly	Asp	Ala	Ala	Lys	Ser	Gln	Ala	Ala	Leu	Asn
	50					55					60				
Pro	His	Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe
65					70				75					80	
Ala	Asp	Thr	Thr	Val	Gln	Ser	Asp	Met	Lys	His	Trp	Pro	Phe	Arg	Val
				85					90					95	
Val	Ser	Glu	Gly	Gly	Lys	Pro	Lys	Val	Pro	Val	Ser	Tyr	Arg	Gly	Glu
		100						105					110		
Asp	Lys	Thr	Phe	Tyr	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Ser	Lys
	115					120						125			
Met	Lys	Glu	Thr	Ala	Glu	Ala	Tyr	Leu	Gly	Gln	Pro	Val	Lys	His	Ala
130					135						140				
Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ser	Gln	Arg	Gln	Ala	Thr
145					150				155					160	
Lys	Asp	Ala	Gly	Ala	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Ile	Asn
			165					170						175	
Glu	Pro	Thr	Ala	Ala	Ala	Ile	Ala	Tyr	Gly	Leu	Asp	Arg	Arg	Gly	Ala
			180					185					190		
Gly	Glu	Arg	Asn	Val	Leu	Ile	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp
	195						200					205			
Val	Ser	Val	Leu	Ser	Ile	Asp	Ala	Gly	Val	Phe	Glu	Val	Lys	Ala	Thr
210						215					220				
Ala	Gly	Asp	Thr	His	Leu	Gly	Gly	Glu	Asp	Phe	Asp	Asn	Arg	Leu	Val
225					230				235					240	
Asn	His	Phe	Met	Glu	Glu	Phe	Arg	Arg	Lys	His	Gly	Lys	Asp	Leu	Ser
			245						250					255	
Gly	Asn	Lys	Arg	Ala	Leu	Gly	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg	Ala
		260						265					270		
Lys	Arg	Thr	Leu	Ser	Ser	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Ile	Asp	Ser
	275						280					285			
Leu	Phe	Glu	Gly	Val	Asp	Phe	Tyr	Thr	Ser	Ile	Thr	Arg	Ala	Arg	Phe
	290					295					300				
Glu	Glu	Leu	Cys	Ser	Asp	Leu	Phe	Arg	Ser	Thr	Leu	Glu	Pro	Val	Glu
305					310					315				320	
Lys	Ala	Leu	Arg	Asp	Ala	Lys	Leu	Asp	Lys	Ala	Gln	Ile	His	Asp	Val
			325						330					335	
Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln	Lys	Leu	Leu
		340						345					350		
Gln	Asp	Phe	Phe	Asn	Gly	Lys	Glu	Leu	Asn	Lys	Ser	Ile	Asn	Pro	Asp
		355					360						365		

Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Val Leu Met Gly
 370 375 380
 Asp Lys Cys Glu Lys Val Gln Asp Leu Leu Leu Leu Asp Val Ala Pro
 385 390 395 400
 Leu Ser Leu Gly Leu Glu Thr Ala Gly Gly Val Met Thr Thr Leu Ile
 405 410 415
 Gln Arg Asn Ala Thr Ile Pro Thr Lys Gln Thr Gln Thr Phe Thr Thr
 420 425 430
 Tyr Ser Asp Asn Gln Pro Gly Val Phe Ile Gln Val Tyr Glu Gly Glu
 435 440 445
 Arg Ala Met Thr Lys Asp Asn Asn Leu Leu Gly Arg Phe Glu Leu Ser
 450 455 460
 Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe
 465 470 475 480
 Asp Ile Asp Ala Asn Gly Ile Leu Ser Val Thr Ala Thr Asp Arg Ser
 485 490 495
 Thr Gly Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu
 500 505 510
 Ser Lys Glu Glu Val Glu Arg Met Val His Glu Ala Glu Gln Tyr Lys
 515 520 525
 Ala Glu Asp Glu Ala Gln Arg Asp Arg Val Ala Ala Lys Asn Ser Leu
 530 535 540
 Glu Ala His Val Phe His Val Lys Gly Ser Leu Gln Glu Glu Ser Leu
 545 550 555 560
 Arg Asp Lys Ile Pro Glu Glu Asp Arg Arg Lys Met Gln Asp Lys Cys
 565 570 575
 Arg Glu Val Leu Ala Trp Leu Glu His Asn Gln Leu Ala Glu Lys Glu
 580 585 590
 Glu Tyr Glu His Gln Lys Arg Glu Leu Glu Gln Ile Cys Arg Pro Ile
 595 600 605
 Phe Ser Arg Leu Tyr Gly Gly Pro Gly Val Pro Gly Gly Ser Ser Cys
 610 615 620
 Gly Thr Gln Ala Arg Gln Gly Asp Pro Ser Thr Gly Pro Ile Ile Glu
 625 630 635 640
 Glu Val Asp

<210> 12
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 <212> DNA
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34

<210> 13
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<400> 13
 gaagctcgag tcaatcaacc tcctcaatga

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<400> 14
tgacaagctt agaattcttc catgaagtgg t

31

<210> 15
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<400> 15
Cys Arg Asp Lys Ile Pro Glu Glu Asp Arg Arg Lys Met Gln
1 5 10